

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Suerbaum, Sebastian
Labigne, Agnes
- (ii) TITLE OF INVENTION: Cloning and Characterization of the flbA
Gene of H. Pylori, Production of Aflagellate Strains
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
(B) STREET: 1300 I Street, N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005-3315
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/015,078
(B) FILING DATE: 29-JAN-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Meyers, Kenneth J.
(B) REGISTRATION NUMBER: 25,146
(C) REFERENCE/DOCKET NUMBER: 02356.0073-01000
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 408-4000
(B) TELEFAX: (202) 408-4400

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:



ATGCCNGGNA AAGCARATG

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

RAAYTTCATN GCNCCRTC

18

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCCAGGAA AGCAAATGGC GATTGATGCG GATTTAAATT CAGGGCTTAT TGATGATAAG	60
GAAGCTAAAA AACGGCGCGC CGCTCTAAGC CAAGAAGCGG ATTTTATGG TGCGATGGAT	120
GGCGCGTCTA AATTT	135

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGATCCGT GGTACTAAT GGTCTAC

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ATGGCCTCTT CAGAGACC

28

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTTTTTTG TGCCATACTT TTAAACTTTA TATTATAATA AGAGACAAAC ACACCTACCA	60
AAATTAAGGC ATTGATTTTA GATTATGGCA AACGAACGCT CCAAATTAGC TTTTAAAAAG	120
ACTTTCCCTG TCTTTAAACG CTTCTTGCAA TCCAAAGACT TAGCCCTTGT GGTCTTTGTG	180
ATAGCGATTT TAGCGATCAT TATCGTGCCG TTACCGCCTT TTGTGTTGGA TTTTTTACTC	240
ACGATTTCTA TCGCGCTATC GGTGTTGATT ATTTTAATCG GGCTTTATAT TGACAAACCG	300
ACTGATTTTA GCGCTTTCCC CACTTTATTA CTCATTGTAA CCTTATACCG CTTGGCTTTA	360
AATGTCGCCA CCACTAGAAT GATTTTAACC CAAGGCTATA AAGGGCCTAG CGCGGTGAGC	420
ATTATTATCA CGGCGTTTGG GGAATTTAGC GTGAGCGGGA ATTATGTGAT TGGGGCTATT	480
ATCTTTAGTA TTTTAGTGCT GGTGAATTTA TTAGTGGTTA CTAATGGTTC TACTAGGGTT	540
ACTGAAGTTA GGGCGCGATT TGCCCTAGAC GCTATGCCAG GAAAGCAAAT GGCGATTGAT	600
GCGGATTTAA ATTCAGGGCT TATTGATGAT AAGGAAGCTA AAAAACGGCG CGCCGCTCTA	660
AGCCAAGAAG CGGATTTTTA TGGTGCGATG GATGGCGCGT CTAAATTTGT CAAAGGCGAT	720
GCGATCGCTT CTATCATTAT CACGCTTATC AATATCATTG GGGGTTTTTT AGTGGGCGTG	780

TTCCAAAGGG ATATGAGCTT GAGCTTTAGT GCTAGCACTT TCACTATCTT AACCATTGGC	840
GATGGGCTTG TAGGGCAAAT CCCTGCCTTA ATCATTGCGA CACGGACCGG TATTGTCGCC	900
ACTCGCACCA CGCAAAACGA AGAAGAGGAC TTTGCTTCTA AGCTCATCAC ACAGCTCACC	960
AATAAAAGCA AAACCTTTAGT GATTGTGGGG GCGATTTATT GCTTTTGCAC CATTCTGGA	1020
CTCCCTACCT TTTCTTTAGC GTTTGTAGGG GCTCTCTTTT TATTCATCGC ATGGCTGATT	1080
AGCAGGGAGG GAAAGGACGG GTTGCTCACT AAATTAGAAA ATTATTTGAG TCAAAAATTC	1140
GGCTTGGAAT TGAGCGAAAA ACCCCACAGC TCCAAAATCA AACCCACGC CCCCACCACA	1200
AGGGCTAAAA CCAAGAAGA GATTAAAAGA GAAGAAGAGC AAGCCATTGA TGAAGTGTTA	1260
AAAATTGAAT TTTTAGAATT GGCTTTAGGC TATCAGCTCT ACAGCTTAGC GGACATGAAA	1320
CAAGGGGGCG ATTTGTTAGA AAGGATTAGG GGTATTAGAA AAAAGATAGC GAGCGATTAT	1380
GGTTTTTTGA TGCCTCAAAT TAGGATTAGG GATAATTTAC AACTCCCCC AACGCATTAT	1440
GAAATCAAGC TTAAGGGCAT TGTGATTGGT GAAGGCATGG TGATGCCGGA TAAGTTTTTA	1500
GCCATGAATA CCGGTTTTGT GAATAAAGAA ATTGAAGGCA TTCCTACTAA AGAGCCGGCT	1560
TTTGGAATGG ACGCTTTATG GATTGAACT AAAAATAAAG AAGAAGCCAT CATTCAAGGC	1620
TATACCATTA TTGATCCAAG CACCGTTATT GCGACGCACA CCAGCGAATT AGTGAAAAAA	1680
TACGCTGAAG ATTTTATCAC TAAAGATGAA GTGAAATCCC TTTTAGAGCG CTTGGCCAAA	1740
GACTATCCTA CGATTGTAGA AGAGAGTAAA AAAATCCCCA CCGGTGCGAT CCGATCAGTC	1800
TTGCAAGCCT TGTTGCATGA AAAAATCCCC ATTAAAGACA TGCTCACTAT TTTAGAAACG	1860
ATTACCGATA TTGCGCCATT AGTTCAAAAC GATGTGAATA TCTTAACCGA ACAAGTGAGG	1920
GCGAGGCTTT CTAGGGTGAT CACTAACGCT TTAAATCTG AAGACGGGCG TTTGAAATTT	1980
TTAACCTTTT CTACCGATAG CGAACAATTT TTGCTTAATA AATTGCGAGA AAATGGCACT	2040
TCTAAGAGCC TACTACTCAA TGTGGGCGAA TTGCAAAAAC TCATTGAAGC GGTCTCTGAA	2100
GAGGCCATGA AAGTCTTGCA AAAAGGGATC GCTCCGGTGA TTTTGATCGT AGAGCCTAAT	2160
TTAAGAAAAG CCCTTTCTAA TCAAATGGAG CAGGCTAGGA TTGATGTAAT CGTGCTAAGC	2220
CATGCTGAAT TAGATCCTAA CTCTAATTTT GAAGCCTTAG GCACGATCCA TATTAACTTT	2280
TAAGGGATAA ATAATTGATA AAAAAGGAGA ATGATGCAAG TTTATCACCT TTCACACATT	2340
GATTTAGACG GCTATGCATG CCAGCTTGTT TCAAAACAAT TTTTAAAAA TATCCAATGC	2400
TATAACGCTA ATTACGGGCG TGAAGTCTCA GCGAGAATTT ATGAGATTTT AAACGCGATC	2460
GCTCAATCTA AAGAGAGTGA ATTCCTTATT TTGATTAGCG A	2501

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
1           5           10           15

Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
20           25           30

Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu
35           40           45

Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu
50           55           60

Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr
65           70           75           80

Leu Leu Leu Ile Val Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr
85           90           95

Thr Arg Met Ile Leu Thr Gln Gly Tyr Lys Gly Pro Ser Ala Val Ser
100          105          110

Ile Ile Ile Thr Ala Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val
115          120          125

Ile Gly Ala Ile Ile Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val
130          135          140

Val Thr Asn Gly Ser Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala
145          150          155          160

Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn
165          170          175

Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu
180          185          190

Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe
195          200          205

Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile
210          215          220

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Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser
 225 230 235 240
 Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Ala Gly Leu Val
 245 250 255
 Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Arg Thr Gly Ile Val Ala
 260 265 270
 Thr Arg Thr Thr Gln Asn Glu Glu Glu Asp Phe Ala Ser Lys Leu Ile
 275 280 285
 Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile
 290 295 300
 Tyr Cys Phe Cys Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala Phe
 305 310 315 320
 Val Gly Ala Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu Gly
 325 330 335
 Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys Phe
 340 345 350
 Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro His
 355 360 365
 Ala Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Ile Lys Arg Glu Glu
 370 375 380
 Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu Ala
 385 390 395 400
 Leu Gly Thr Gln Leu Tyr Ser Leu Ala Asp Met Lys Gln Gly Gly Asp
 405 410 415
 Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp Tyr
 420 425 430
 Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu Pro
 435 440 445
 Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu Gly
 450 455 460
 Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
 465 470 475 480
 Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
 485 490 495
 Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
 500 505 510
 Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
 515 520 525

Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
 530 535 540
 Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
 545 550 555 560
 Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
 565 570 575
 Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
 580 585 590
 Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
 595 600 605
 Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
 610 615 620
 Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
 625 630 635 640
 Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
 645 650 655
 Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
 660 665 670
 Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
 675 680 685
 Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
 690 695 700
 Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
 705 710 715 720
 Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
 725 730

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
 1 5 10 15

Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
 20 25 30
 Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu
 35 40 45
 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu
 50 55 60
 Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr
 65 70 75 80
 Leu Leu Leu Ile Val Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr
 85 90 95
 Thr Arg Met Ile Leu Thr Gln Gly Tyr Lys Gly Pro Ser Ala Val Ser
 100 105 110
 Ile Ile Ile Thr Ala Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val
 115 120 125
 Ile Gly Ala Ile Ile Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val
 130 135 140
 Val Thr Asn Gly Ser Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala
 145 150 155 160
 Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn
 165 170 175
 Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu
 180 185 190
 Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe
 195 200 205
 Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile
 210 215 220
 Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser
 225 230 235 240
 Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Asp Gly Leu Val
 245 250 255
 Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Arg Thr Gly Ile Val Ala
 260 265 270
 Thr Arg Thr Thr Gln Asn Glu Glu Glu Asp Phe Ala Ser Lys Leu Ile
 275 280 285
 Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile
 290 295 300
 Tyr Cys Phe Cys Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala Phe
 305 310 315 320

Val Gly Ala Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu Gly
 325 330 335
 Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys Phe
 340 345 350
 Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro His
 355 360 365
 Ala Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Ile Lys Arg Glu Glu
 370 375 380
 Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu Ala
 385 390 395 400
 Leu Gly Tyr Gln Leu Tyr Ser Leu Ala Asp Met Lys Gln Gly Gly Asp
 405 410 415
 Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp Tyr
 420 425 430
 Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu Pro
 435 440 445
 Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu Gly
 450 455 460
 Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
 465 470 475 480
 Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
 485 490 495
 Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
 500 505 510
 Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
 515 520 525
 Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
 530 535 540
 Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
 545 550 555 560
 Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
 565 570 575
 Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
 580 585 590
 Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
 595 600 605
 Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
 610 615 620

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9;

Met	Ala	Lys	Asn	Lys	Ile	Val	Asp	Leu	Val	Phe	Pro	Phe	Leu	Gly	Pro
1				5					10					15	
Leu	Ile	Ala	Pro	Val	Leu	Lys	Ala	Lys	Ser	Leu	Thr	Ile	Val	Gly	Phe
			20					25					30		
Leu	Val	Cys	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Ser	Pro	Ile
		35					40					45			
Leu	Asp	Phe	Phe	Leu	Ala	Leu	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile
	50					55					60				
Leu	Ile	Ser	Ile	Tyr	Ile	Pro	Lys	Pro	Thr	Asp	Leu	Thr	Thr	Phe	Pro
65					70					75					80
Thr	Leu	Ile	Leu	Ile	Ile	Thr	Leu	Phe	Arg	Leu	Ser	Leu	Asn	Ile	Ala
				85					90					95	
Thr	Thr	Arg	Met	Ile	Leu	Ser	Glu	Gly	Gln	Asn	Gly	Pro	Glu	Ala	Val
			100					105					110		

Ser Glu Ile Ile Ala Ala Phe Gly Glu Phe Val Val Gly Gly Asn Met
 115 120 125
 Val Ile Gly Val Ile Val Phe Cys Ile Leu Val Leu Ile Asn Phe Met
 130 135 140
 Val Val Thr Lys Gly Ser Thr Arg Val Ser Glu Val Gln Ala Arg Phe
 145 150 155 160
 Thr Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu
 165 170 175
 Asn Ala Gly Leu Ile Asp Glu Gln Thr Ala Arg Ala Arg Arg Gln Glu
 180 185 190
 Val Ile Ala Glu Ala Asn Phe Tyr Gly Ala Met Asp Gly Ser Ser Lys
 195 200 205
 Phe Ile Lys Gly Asp Ala Val Ala Gly Ile Ile Ile Thr Ile Ile Asn
 210 215 220
 Ile Ile Gly Gly Phe Leu Ile Gly Ser Phe Gln His Asp Met Ala Leu
 225 230 235 240
 Ser Asp Ala Ala Ser Thr Tyr Thr Ile Leu Thr Ile Gly Asp Gly Leu
 245 250 255
 Val Ser Gln Ile Pro Gly Leu Ile Thr Ser Thr Ala Thr Ala Ile Ile
 260 265 270
 Ile Thr Arg Ala Ser Lys Asp Glu Glu Asn Phe Ala Glu Gly Thr Leu
 275 280 285
 Thr Gln Leu Leu Ser Glu Tyr Arg Thr Leu Leu Ile Val Gly Phe Val
 290 295 300
 Leu Phe Ile Phe Ala Leu Val Pro Gly Leu Pro Thr Leu Ser Leu Gly
 305 310 315 320
 Phe Met Ala Leu Val Phe Leu Ser Leu Gly Tyr Leu Tyr Lys Gln Val
 325 330 335
 Lys Glu Gly Lys Ile Asp Ile Thr Thr Val Lys Lys Ser Lys Pro Ser
 340 345 350
 Ala Ala Val Ala Ser Gln Ser Gly Ala Gly Gly Thr Thr Ala Ala Pro
 355 360 365
 Ala Lys Lys Ser Glu Glu Glu Ile Leu Lys Glu Glu Glu His Lys Ile
 370 375 380
 Asn Asp Ile Leu Lys Val Glu Ile Leu Glu Leu Glu Leu Gly Tyr Gly
 385 390 395 400
 Leu Ile Lys Leu Ala Glu Asn Glu Leu Thr Glu Arg Ile Arg Ser Met
 405 410 415

Arg Arg Ser Ile Ala Glu Ser Leu Gly Phe Leu Met Pro Lys Ile Arg
 420 425 430
 Ile Arg Asp Asn Leu Arg Leu Lys Pro Asn Glu Tyr Ser Phe Lys Leu
 435 440 445
 Lys Gly Val Ser Ile Ala Ser Ala Glu Ile Tyr Pro Asp Lys Tyr Leu
 450 455 460
 Ala Met Asp Ser Gly Phe Ile Thr Glu Glu Ile Glu Gly Ile Ala Thr
 465 470 475 480
 Lys Glu Pro Ala Phe Asn Ser Asp Ala Leu Trp Ile Asp Ala Asn Leu
 485 490 495
 Lys Asp Glu Ala Thr Leu Asn Gly Tyr Ile Val Ile Asp Pro Ala Ser
 500 505 510
 Val Ile Ser Thr His Met Ser Glu Leu Ala Lys Ala His Ala Ser Glu
 515 520 525
 Leu Leu Thr Arg Gln Glu Val Gln Asn Leu Leu Asp Lys Val Lys Asn
 530 535 540
 Asp Tyr Pro Ile Ile Val Glu Gly Ala Leu Gly Val Ala Pro Val Ser
 545 550 555 560
 Leu Ile Gln Lys Ile Leu Lys Asp Leu Leu Lys His His Ile Pro Ile
 565 570 575
 Lys Asp Met Leu Thr Ile Leu Glu Ser Val Ser Asp Ile Ala Glu Val
 580 585 590
 Ser Lys Ser Phe Asp Met Ile Ile Glu His Val Arg Ala Ser Leu Ala
 595 600 605
 Arg Met Ile Thr Asn Met Tyr Leu Asp Asp Lys Gly Asn Leu Asp Ile
 610 615 620
 Phe Ile Leu Asp Ser Ala Ser Ser Ala Val Leu Met Glu Asn Val Gln
 625 630 635 640
 Phe Arg Asp Gly Ser Tyr His Leu Pro Leu Ser Val Ala Gln Thr Gly
 645 650 655
 Thr Leu Val Asp Thr Leu Arg Ala Glu Val Ala Ala Val Ala Asn Gly
 660 665 670
 Arg Ile Lys Pro Phe Ile Leu Cys Val Glu Pro Gln Leu Arg Lys Phe
 675 680 685
 Ile Ala Asp Ile Cys Tyr Asn Phe Ser Ile Asn Ile Val Val Leu Ser
 690 695 700
 Phe Ala Glu Ile Ala Glu Asn Thr Asn Phe Asn Thr Glu Gly Ile Ile
 705 710 715 720
 Arg Ile Glu Leu

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Ala Asp Ala Ala Ala Pro Asn Ala Ser Ser Met Pro Ser Ala Lys
1           5           10           15

Ser Leu Leu Asp Gly Leu Met Arg Gly Glu Met Gly Leu Ala Leu Gly
20           25           30

Val Val Gly Ile Ile Val Leu Leu Ile Ile Pro Val Pro Ala Pro Leu
35           40           45

Leu Asp Val Leu Leu Ala Ile Ser Leu Thr Gly Ser Val Leu Ile Leu
50           55           60

Met Thr Ala Ile Leu Ile Lys Lys Pro Leu Glu Phe Thr Ser Phe Pro
65           70           75           80

Thr Val Leu Leu Val Thr Thr Leu Phe Arg Leu Gly Leu Asn Ile Ala
85           90           95

Ser Thr Arg Leu Ile Leu Ser His Gly Gln Glu Gly Thr Gly Gly Ala
100          105          110

Gly Ala Val Ile Glu Ala Phe Gly His Leu Met Met Gln Gly Asn Phe
115          120          125

Val Ile Gly Val Ile Val Phe Ile Ile Leu Ile Val Val Asn Phe Met
130          135          140

Val Val Thr Lys Gly Ser Gly Arg Ile Ala Glu Val Ala Ala Arg Phe
145          150          155          160

Thr Leu Asp Ser Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu
165          170          175

Ser Thr Gly Leu Ile Ser Gln Asp Glu Ala Lys Ile Arg Arg Lys Glu
180          185          190

Leu Glu Gln Glu Ser Thr Phe Phe Gly Ala Met Asp Gly Ala Ser Lys
195          200          205

Phe Val Lys Gly Asp Ala Ile Ala Gly Leu Ile Ile Thr Ala Ile Asn
210          215          220

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Ile Ile Gly Gly Ile Ile Ile Gly Val Val Gln His Lys Met Pro Phe
 225 230 235 240
 Gly Asp Ala Ala Ser Thr Tyr Thr Ile Met Thr Ile Gly Asp Gly Leu
 245 250 255
 Val Ser Gln Ile Pro Ala Leu Ile Ile Ser Ile Ala Ala Gly Met Val
 260 265 270
 Val Ser Lys Ala Gly Val Glu Gly Ser Ala Asp Lys Ala Leu Thr Thr
 275 280 285
 Gln Leu Ala Met Asn Pro Val Gly Leu Gly Met Val Ser Ala Ser Ser
 290 295 300
 Gly Ile Ile Ala Leu Ile Pro Gly Met Pro Ile Phe Pro Phe Ala Ala
 305 310 315 320
 Met Ala Leu Ala Ala Gly Ala Leu Ala Tyr Lys Arg Val Gln Asp Ala
 325 330 335
 Lys Lys Pro Lys Ala Leu Asp Pro Ala Asp Leu Glu Ala Ala Ala Pro
 340 345 350
 Ser Glu Pro Glu Glu Glu Pro Ile Ser Ala Ser Leu Ala Ile Asp Asp
 355 360 365
 Val Lys Ile Glu Leu Gly Tyr Gly Leu Leu Thr Leu Ile Asn Asp Leu
 370 375 380
 Asp Gly Arg Lys Leu Thr Asp Gln Ile Arg Ala Leu Arg Lys Thr Leu
 385 390 395 400
 Ala Ser Glu Tyr Gly Phe Val Met Pro Pro Val Arg Ile Leu Asp Asn
 405 410 415
 Met Arg Leu Ala Asn Gln Gly Tyr Ala Ile Arg Ile Lys Glu Met Glu
 420 425 430
 Ala Gly Ala Gly Glu Val Arg Leu Gly Cys Leu Met Cys Met Asp Pro
 435 440 445
 Arg Gly Gly Gln Val Glu Leu Pro Gly Glu His Val Arg Glu Pro Ala
 450 455 460
 Phe Gly Leu Pro Ala Thr Trp Ile Ala Asp Asp Leu Arg Glu Glu Ala
 465 470 475 480
 Thr Phe Arg Gly Tyr Thr Val Val Asp Pro Ala Thr Val Leu Thr Thr
 485 490 495
 His Leu Thr Glu Ile Leu Lys Glu Asn Met Ala Asp Leu Leu Ser Tyr
 500 505 510
 Ala Glu Val Gln Lys Leu Leu Lys Glu Leu Pro Glu Thr Gln Lys Lys
 515 520 525

Leu Val Asp Asp Leu Ile Pro Gly Thr Val Thr Ala Thr Thr Val Gln
 530 535 540
 Arg Val Leu Gln Ser Leu Leu Arg Glu Arg Val Ser Ile Arg Asp Leu
 545 550 555 560
 Pro Gln Ile Leu Glu Gly Val Gly Glu Ala Ala Pro His Thr Ala Ser
 565 570 575
 Val Thr Gln Leu Val Glu Gln Val Arg Ala Arg Leu Ala Arg Gln Leu
 580 585 590
 Cys Trp Ala Asn Arg Gly Asp Asp Gly Ala Leu Pro Ile Ile Thr Leu
 595 600 605
 Ser Ala Asp Trp Glu Gln Ala Phe Ala Glu Ala Leu Ile Gly Pro Gly
 610 615 620
 Asp Asp Lys Gln Leu Ala Leu Pro Pro Ser Arg Leu Gln Asp Phe Ile
 625 630 635 640
 Arg Gly Val Arg Asp Ser Phe Glu Arg Ala Ala Leu Ala Gly Glu Ala
 645 650 655
 Pro Val Leu Leu Thr Ser Pro Gly Val Arg Pro Tyr Val Arg Ser Ile
 660 665 670
 Ile Glu Arg Phe Arg Gly Gln Thr Val Val Met Ser Gln Asn Glu Ile
 675 680 685
 His Pro Arg Ala Arg Leu Lys Thr Val Gly Met Val
 690 695 700

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Pro His Asp Leu Glu Trp Leu Asn Arg Ile Gly Glu Arg Lys
 1 5 10 15
 Asp Ile Met Leu Ala Val Leu Leu Leu Ala Val Val Phe Met Met Val
 20 25 30
 Leu Pro Leu Pro Pro Leu Val Leu Asp Ile Leu Ile Ala Val Asn Met
 35 40 45

Thr Ile Ser Val Val Leu Leu Met Ile Ala Ile Tyr Ile Asn Ser Pro
 50 55 60
 Leu Gln Phe Ser Ala Phe Pro Ala Val Leu Leu Val Thr Thr Leu Phe
 65 70 75 80
 Arg Leu Ala Leu Ser Val Ser Thr Thr Arg Met Ile Leu Leu Gln Ala
 85 90 95
 Asp Ala Gly Gln Ile Val Tyr Thr Phe Gly Asn Phe Val Val Gly Gly
 100 105 110
 Asn Leu Ile Val Gly Ile Val Ile Phe Leu Ile Ile Thr Ile Val Gln
 115 120 125
 Phe Leu Val Ile Thr Lys Gly Ser Glu Arg Val Ala Glu Val Ser Ala
 130 135 140
 Arg Phe Ser Leu Asp Ala Met Pro Gly Lys Gln Met Ser Ile Asp Gly
 145 150 155 160
 Asp Met Arg Ala Gly Val Ile Asp Val Asn Glu Ala Arg Glu Arg Arg
 165 170 175
 Ala Thr Ile Glu Lys Glu Ser Gln Met Phe Gly Ser Met Asp Gly Ala
 180 185 190
 Met Lys Phe Val Lys Gly Asp Ala Ile Ala Gly Leu Ile Ile Ile Phe
 195 200 205
 Val Asn Ile Leu Gly Gly Val Thr Ile Gly Val Thr Gln Lys Gly Leu
 210 215 220
 Ala Ala Ala Glu Ala Leu Gln Leu Tyr Ser Ile Leu Thr Val Gly Asp
 225 230 235 240
 Gly Met Val Ser Gln Val Pro Ala Leu Leu Ile Ala Ile Thr Ala Gly
 245 250 255
 Ile Ile Val Thr Arg Val Ser Ser Glu Asp Ser Ser Asp Leu Gly Ser
 260 265 270
 Asp Ile Gly Lys Gln Val Val Ala Gln Pro Lys Ala Met Leu Ile Gly
 275 280 285
 Gly Val Leu Leu Leu Leu Phe Gly Leu Ile Pro Gly Phe Pro Thr Val
 290 295 300
 Thr Phe Leu Ile Leu Ala Leu Leu Val Gly Cys Gly Gly Tyr Met Leu
 305 310 315 320
 Ser Arg Lys Gln Ser Arg Asn Asp Glu Ala Asn Gln Asp Leu Gln Ser
 325 330 335
 Ile Leu Thr Ser Gly Ser Gly Ala Pro Ala Ala Arg Thr Lys Ala Lys
 340 345 350

Thr Ser Gly Ala Asn Lys Gly Arg Leu Gly Glu Gln Glu Ala Phe Ala
 355 360 365
 Met Thr Val Pro Leu Leu Ile Asp Val Asp Ser Ser Gln Gln Glu Ala
 370 375 380
 Leu Glu Ala Asn Ala Leu Asn Asp Glu Leu Val Arg Val Arg Arg Ala
 385 390 395 400
 Leu Tyr Leu Asp Leu Gly Val Pro Phe Pro Gly Ile His Leu Arg Phe
 405 410 415
 Asn Glu Gly Met Gly Glu Gly Glu Tyr Ile Ile Ser Leu Gln Glu Val
 420 425 430
 Pro Val Ala Arg Gly Glu Leu Lys Ala Gly Tyr Leu Leu Val Arg Glu
 435 440 445
 Ser Val Ser Gln Leu Glu Leu Leu Gly Ile Pro Tyr Glu Lys Gly Glu
 450 455 460
 His Leu Leu Pro Asp Gln Glu Ala Phe Trp Val Ser Val Glu Tyr Glu
 465 470 475 480
 Glu Arg Leu Glu Lys Ser Gln Leu Glu Phe Phe Ser His Ser Gln Val
 485 490 495
 Leu Thr Trp His Leu Ser His Val Leu Arg Glu Tyr Ala Glu Asp Phe
 500 505 510
 Ile Gly Ile Gln Glu Thr Arg Tyr Leu Leu Glu Gln Met Glu Gly Gly
 515 520 525
 Tyr Gly Glu Leu Ile Lys Glu Val Gln Arg Ile Val Pro Leu Gln Arg
 530 535 540
 Met Thr Glu Ile Leu Gln Arg Leu Val Gly Glu Asp Ile Ser Ile Arg
 545 550 555 560
 Asn Met Arg Ser Ile Leu Glu Ala Met Val Glu Trp Gly Gln Lys Glu
 565 570 575
 Lys Asp Val Val Gln Leu Thr Glu Tyr Ile Arg Ser Ser Leu Lys Arg
 580 585 590
 Tyr Ile Cys Tyr Lys Tyr Ala Asn Gly Asn Asn Ile Leu Pro Ala Tyr
 595 600 605
 Leu Phe Asp Gln Glu Val Glu Glu Lys Ile Arg Ser Gly Val Arg Gln
 610 615 620
 Thr Ser Ala Gly Ser Tyr Leu Ala Leu Glu Pro Ala Val Thr Glu Ser
 625 630 635 640
 Leu Leu Glu Gln Val Arg Lys Thr Ile Gly Asp Leu Ser Gln Ile Gln
 645 650 655

Ser Lys Pro Val Leu Ile Val Ser Met Asp Ile Arg Arg Tyr Val Arg
 660 665 670

Lys Leu Ile Glu Ser Glu Tyr Tyr Gly Leu Pro Val Leu Ser Tyr Gln
 675 680 685

Glu Leu Thr Gln Gln Ile Asn Ile Gln Pro Leu Gly Arg Ile Cys Leu
 690 695 700

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Leu Leu Ser Leu Leu Asn Ser Ala Arg Leu Arg Pro Glu Leu Leu
 1 5 10 15

Ile Leu Val Leu Met Val Met Ile Ile Ser Met Phe Val Ile Pro Leu
 20 25 30

Pro Thr Tyr Leu Val Asp Phe Leu Ile Ala Leu Asn Ile Val Leu Ala
 35 40 45

Ile Leu Val Phe Met Gly Ser Phe Tyr Ile Asp Arg Ile Leu Ser Phe
 50 55 60

Ser Thr Phe Pro Ala Val Leu Leu Ile Thr Thr Leu Phe Arg Leu Ala
 65 70 75 80

Leu Ser Ile Ser Thr Ser Arg Leu Ile Leu Ile Glu Ala Asp Ala Gly
 85 90 95

Glu Ile Ile Ala Thr Phe Gly Gln Phe Val Ile Gly Asp Ser Leu Ala
 100 105 110

Val Gly Phe Val Val Phe Ser Ile Val Thr Val Val Gln Phe Ile Val
 115 120 125

Ile Thr Lys Gly Ser Glu Arg Val Ala Glu Val Ala Ala Arg Phe Ser
 130 135 140

Leu Asp Gly Met Pro Gly Lys Gln Met Ser Ile Asp Ala Asp Leu Lys
 145 150 155 160

Ala Gly Ile Ile Asp Ala Asp Ala Ala Arg Glu Arg Arg Ser Val Leu
 165 170 175

Glu Arg Glu Ser Gln Leu Tyr Gly Ser Phe Asp Gly Ala Met Lys Phe
 180 185 190
 Ile Lys Gly Asp Ala Ile Ala Gly Ile Ile Ile Ile Phe Val Asn Phe
 195 200 205
 Ile Gly Gly Ile Ser Val Gly Met Thr Arg His Gly Met Asp Leu Ser
 210 215 220
 Ser Ala Leu Ser Thr Tyr Thr Met Leu Thr Ile Gly Asp Gly Leu Val
 225 230 235 240
 Ala Gln Ile Pro Ala Leu Leu Ile Ala Ile Ser Ala Gly Phe Ile Val
 245 250 255
 Thr Arg Val Asn Gly Asp Thr Asp Asn Met Gly Arg Asn Ile Met Thr
 260 265 270
 Gln Leu Leu Asn Asn Pro Phe Val Leu Val Val Thr Ala Ile Leu Thr
 275 280 285
 Ile Ser Met Gly Thr Leu Pro Gly Phe Pro Leu Pro Val Phe Val Ile
 290 295 300
 Leu Ser Val Val Leu Ser Val Leu Phe Tyr Phe Lys Phe Arg Glu Ala
 305 310 315 320
 Lys Arg Ser Ala Ala Lys Pro Lys Thr Ser Lys Gly Glu Gln Pro Leu
 325 330 335
 Ser Ile Glu Glu Lys Glu Gly Ser Ser Leu Gly Leu Ile Gly Asp Leu
 340 345 350
 Asp Lys Val Ser Thr Glu Thr Val Pro Leu Ile Leu Leu Val Pro Lys
 355 360 365
 Ser Arg Arg Glu Asp Leu Glu Lys Ala Gln Leu Ala Glu Arg Leu Arg
 370 375 380
 Ser Gln Phe Phe Ile Asp Tyr Gly Val Arg Leu Pro Glu Val Leu Leu
 385 390 395 400
 Arg Asp Gly Glu Gly Leu Asp Asp Asn Ser Ile Val Leu Leu Ile Asn
 405 410 415
 Glu Ile Arg Val Glu Gln Phe Thr Val Tyr Phe Asp Leu Met Arg Val
 420 425 430
 Val Asn Tyr Ser Asp Glu Val Val Ser Phe Gly Ile Asn Pro Thr Ile
 435 440 445
 His Gln Gln Gly Ser Ser Gln Tyr Phe Trp Val Thr His Glu Glu Gly
 450 455 460
 Glu Lys Leu Arg Glu Leu Gly Tyr Val Leu Arg Asn Ala Leu Asp Glu
 465 470 475 480

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Val Met Ile Ile Ala Met Leu Ile Ile Pro Leu Pro Thr Tyr Leu
1 5 10 15

Val Asp Phe Leu Ile Gly Leu Asn Ile Val Leu Ala Ile Leu Val Phe
 20 25 30
 Met Gly Ser Phe Tyr Ile Glu Arg Ile Leu Ser Phe Ser Thr Phe Pro
 35 40 45
 Ser Val Leu Leu Ile Thr Thr Leu Phe Arg Leu Ala Leu Ser Ile Ser
 50 55 60
 Thr Ser Arg Leu Ile Leu Val Asp Ala Asp Arg Gly Lys Ile Ile Thr
 65 70 75 80
 Thr Phe Gly Gln Phe Val Ile Gly Asp Ser Leu Ala Val Gly Phe Val
 85 90 95
 Ile Phe Ser Ile Val Thr Val Val Gln Phe Ile Val Ile Thr Lys Gly
 100 105 110
 Ser Glu Arg Val Ala Glu Val Ala Ala Arg Phe Ser Leu Asp Gly Met
 115 120 125
 Pro Gly Lys Gln Met Ser Ile Asp Ala Asp Leu Lys Ala Gly Ile Ile
 130 135 140
 Asp Ala Ala Gly Ala Lys Glu Arg Arg Ser Ile Leu Glu Arg Glu Ser
 145 150 155 160
 Gln Leu Tyr Gly Ser Phe Asp Gly Ala Met Lys Phe Ile Lys Gly Asp
 165 170 175
 Ala Ile Ala Gly Ile Ile Ile Ile Phe Val Asn Leu Ile Gly Gly Ile
 180 185 190
 Ser Val Gly Met Ser Gln His Gly Met Ser Leu Ser Gly Ala Leu Ser
 195 200 205
 Thr Tyr Thr Ile Leu Thr Ile Gly Asp Gly Leu Val Ser Gln Ile Pro
 210 215 220
 Ala Leu Leu Ile Ser Ile Ser Ala Gly Phe Met Leu Thr Arg Val Asn
 225 230 235 240
 Gly Asp Ser Asp Asn Met Gly Arg Asn Ile Met Ser Gln Ile Phe Gly
 245 250 255
 Asn Pro Phe Val Leu Ile Val Thr Ser Ala Leu Ala Leu Ala Ile Gly
 260 265 270
 Met Leu Pro Gly Phe Pro Phe Phe Val Phe Phe Leu Ile Ala Val Thr
 275 280 285
 Leu Thr Ala Leu Phe Tyr Tyr Lys Lys Val Val Glu Lys Glu Lys Ser
 290 295 300
 Leu Ser Glu Ser Asp Ser Ser Gly Tyr Thr Gly Thr Phe Asp Ile Asp
 305 310 315 320

Asn Thr His Asp Ser Ser Leu Ala Met Ile Glu Asn Leu Asp Arg Ile
 325 330 335
 Ser Ser Glu Thr Val Pro Leu Ile Leu Leu Phe Ala Glu Asn Lys Ile
 340 345 350
 Asn Ala Asn Asp Met Glu Gly Leu Ile Glu Arg Ile Arg Ser Gln Phe
 355 360 365
 Phe Ile Asp Tyr Gly Val Arg Leu Pro Thr Ile Leu Tyr Arg Thr Ser
 370 375 380
 Asn Glu Leu Lys Val Asp Asp Ile Val Leu Leu Ile Asn Glu Val Arg
 385 390 395 400
 Ala Asp Ser Phe Asn Ile Tyr Phe Asp Lys Val Cys Ile Thr Asp Glu
 405 410 415
 Asn Gly Asp Ile Asp Ala Leu Gly Ile Pro Val Val Ser Thr Ser Tyr
 420 425 430
 Asn Glu Arg Val Ile Ser Trp Val Asp Val Ser Tyr Thr Glu Asn Leu
 435 440 445
 Thr Asn Ile Asp Ala Lys Ile Lys Ser Ala Gln Asp Glu Phe Tyr His
 450 455 460
 Gln Leu Ser Gln Ala Leu Leu Asn Asn Ile Asn Glu Ile Phe Gly Ile
 465 470 475 480
 Gln Glu Thr Lys Asn Met Leu Asp Gln Phe Glu Asn Arg Tyr Pro Asp
 485 490 495
 Leu Leu Lys Glu Val Phe Arg His Val Thr Ile Gln Arg Ile Ser Glu
 500 505 510
 Val Leu Gln Arg Leu Leu Gly Glu Asn Ile Ser Val Arg Asn Leu Lys
 515 520 525
 Leu Ile Met Glu Ser Leu Ala Leu Trp Ala Pro Arg Glu Lys Asp Val
 530 535 540
 Ile Thr Leu Val Glu His Val Arg Ala Ser Leu Ser Arg Tyr Ile Cys
 545 550 555 560
 Ser Lys Ile Ala Val Ser Gly Glu Ile Lys Val Val Met Leu Ser Gly
 565 570 575
 Tyr Ile Glu Asp Ala Ile Arg Lys Gly Ile Arg Gln Thr Ser Gly Gly
 580 585 590
 Ser Phe Leu Asn Met Asp Ile Glu Val Ser Asp Glu Val Met Glu Thr
 595 600 605
 Leu Ala His Ala Leu Arg Glu Leu Arg Asn Ala Lys Lys Asn Phe Val
 610 615 620

Leu Leu Val Ser Val Asp Ile Arg Arg Phe Val Lys Arg Leu Ile Asp
625 630 635 640

Asn Arg Phe Lys Ser Ile Leu Val Ile Ser Tyr Ala Glu Ile Asp Glu
645 650 655

Ala Tyr Thr Ile Asn Val Leu Lys Thr Ile
660 665